

SI TABLE S3
Relative expression ratios of significantly-changed proteins in PC3-LN4 cells by 24-hr drug treatments
(10 altered proteins that were common for all treated groups are highlighted with shadow)

Accession Number	Protein Name	KX01 treatment			KX02 treatment			Vinblastine treatment		
		Ratio	StdDev	p Value	Ratio	StdDev	p Value	Ratio	StdDev	p Value
Q92597	Protein NDRG1	1.46	0.13	< 0.01	1.60	0.24	< 0.01	1.85	0.27	< 0.01
Q12774	Rho guanine nucleotide exchange factor 5	1.60	0.11	< 0.01	1.57	0.16	< 0.01	1.58	0.33	< 0.01
Q16763	Ubiquitin-conjugating enzyme E2 S	1.89	0.13	< 0.01	1.88	0.20	< 0.01	1.44	0.24	< 0.01
P16989	DNA-binding protein A	0.35	0.02	< 0.01	0.55	0.05	< 0.01	0.53	0.06	< 0.01
Q27J81	Inverted formin-2	0.56	0.14	< 0.01	0.54	0.14	< 0.01	0.60	0.39	0.04
P10412	Histone H1.4	0.57	0.02	< 0.01	0.59	0.04	< 0.01	0.66	0.06	< 0.01
Q9BYG3	MKI67 FHA domain-interacting nucleolar phosphoprotein	0.59	0.19	0.04	0.53	0.20	0.01	0.68	0.43	0.25
Q9Y314	Nitric oxide synthase-interacting protein	0.61	0.04	< 0.01	0.60	0.11	< 0.01	0.71	0.17	< 0.01
Q9H3H3	Uncharacterized protein C11orf68	0.67	0.14	< 0.01	0.68	0.22	< 0.01	0.66	0.25	< 0.01
Q9BQG0	Myb-binding protein 1A	0.69	0.09	< 0.01	0.54	0.10	< 0.01	0.62	0.14	< 0.01
O00541	Pescadillo homolog 1	0.79	0.14	< 0.01	0.71	0.20	< 0.01	0.69	0.37	0.42
O00567	Nucleolar protein 5A	0.89	0.15	0.63	0.79	0.19	< 0.01	0.64	0.21	0.03
O14744	Protein arginine N-methyltransferase 5	1.49	0.34	0.03	1.26	0.31	0.12	1.11	0.28	< 0.01
O14893	Survival of motor neuron protein-interacting protein 1	2.89	1.65	< 0.01	1.21	1.14	1.00	0.84	0.45	1.00
O14929	Histone acetyltransferase type B catalytic subunit	0.53	0.17	< 0.01	0.58	0.21	< 0.01	0.73	0.63	0.71
O15067	Phosphoribosylformylglycinamide synthase	1.40	0.32	0.01	1.31	0.42	0.25	0.69	0.49	0.03
O15144	Actin-related protein 2/3 complex subunit 2	0.89	0.23	0.82	0.88	0.25	0.43	0.12	0.07	0.02
O43491	Band 4.1-like protein 2	0.82	0.23	0.07	0.65	0.23	< 0.01	0.91	0.51	0.33
O43776	Asparaginyl-tRNA synthetase, cytoplasmic	0.84	0.15	0.18	0.90	0.19	0.02	0.58	0.22	< 0.01
O60216	Double-strand-break repair protein rad21 homolog	1.47	0.24	< 0.01	1.20	0.27	0.32	1.17	0.27	< 0.01
O60232	Sjogren syndrome/scleroderma autoantigen 1	0.50	0.26	< 0.01	0.75	0.42	< 0.01	0.39	0.33	< 0.01
O75131	Copine-3	0.82	0.08	< 0.01	0.82	0.19	< 0.01	0.67	0.30	< 0.01
O75683	Surfeit locus protein 6	0.60	0.11	< 0.01	0.71	0.19	0.02	0.77	0.18	< 0.01
O75694	Nuclear pore complex protein Nup155	0.70	0.13	0.02	0.73	0.16	< 0.01	0.64	0.27	0.02
O95400	CD2 antigen cytoplasmic tail-binding protein 2	0.96	0.19	0.98	0.83	0.28	0.35	0.02	0.02	< 0.01
O95864	Fatty acid desaturase 2	0.38	0.18	< 0.01	0.53	0.23	0.02	0.76	0.62	0.79
P00403	Cytochrome c oxidase subunit 2	1.52	0.52	< 0.01	1.33	0.48	< 0.01	1.19	0.46	< 0.01
P02533	Keratin, type I cytoskeletal 14	0.81	0.06	< 0.01	2.16	0.79	< 0.01	0.89	0.16	< 0.01
P02768	Serum albumin	0.79	0.21	0.13	0.68	0.19	< 0.01	0.55	0.29	< 0.01
P04264	Keratin, type II cytoskeletal 1	0.49	0.05	< 0.01	1.07	0.35	< 0.01	0.93	0.22	0.43

P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	1.51	0.31	< 0.01	1.09	0.30	1.00	1.04	0.33	< 0.01
P06493	Cell division control protein 2 homolog	0.80	0.05	< 0.01	0.90	0.08	< 0.01	0.70	0.06	< 0.01
P06737	Glycogen phosphorylase, liver form	0.80	0.14	0.15	0.81	0.18	< 0.01	0.65	0.22	< 0.01
P06748	Nucleophosmin	1.70	0.30	< 0.01	1.50	0.34	< 0.01	0.91	0.21	< 0.01
P07437	Tubulin beta chain	0.70	0.02	< 0.01	0.80	0.04	< 0.01	0.67	0.07	< 0.01
P08754	Guanine nucleotide-binding protein G(k) subunit alpha	0.84	0.06	< 0.01	0.69	0.13	< 0.01	0.83	0.18	< 0.01
P08779	Keratin, type I cytoskeletal 16	0.81	0.07	< 0.01	2.19	0.82	< 0.01	0.83	0.17	0.05
P09234	U1 small nuclear ribonucleoprotein C	0.68	0.13	< 0.01	0.64	0.26	< 0.01	0.77	0.52	1.00
P11766	Alcohol dehydrogenase class-3	1.38	0.65	0.23	1.44	0.79	0.18	1.41	0.70	< 0.01
P12268	Inosine-5'-monophosphate dehydrogenase 2	1.17	0.13	0.24	1.08	0.13	< 0.01	0.64	0.12	< 0.01
P17301	Integrin alpha-2	1.53	0.14	< 0.01	1.22	0.27	0.15	1.06	0.21	< 0.01
P17480	Nucleolar transcription factor 1	0.66	0.26	0.08	0.69	0.33	0.05	0.76	0.53	0.73
P20290	Transcription factor BTF3	0.62	0.10	< 0.01	0.75	0.10	< 0.01	0.74	0.15	< 0.01
P20618	Proteasome subunit beta type-1	1.43	0.34	< 0.01	1.23	0.38	0.60	1.06	0.30	< 0.01
P20674	Cytochrome c oxidase subunit 5A, mitochondrial	1.53	0.54	< 0.01	1.17	0.48	1.00	0.97	0.42	0.41
P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	1.41	0.16	< 0.01	1.19	0.23	0.02	1.21	0.32	< 0.01
P22681	E3 ubiquitin-protein ligase CBL	3.75	8.78	0.25	1.94	3.82	0.80	0.18	0.28	< 0.01
P23588	Eukaryotic translation initiation factor 4B	1.41	0.10	< 0.01	1.27	0.11	< 0.01	1.17	0.21	< 0.01
P25685	DnaJ homolog subfamily B member 1	0.67	0.09	< 0.01	0.83	0.13	< 0.01	0.92	0.27	0.48
P26358	DNA (cytosine-5)-methyltransferase 1	1.09	0.67	0.97	0.65	0.28	< 0.01	0.67	0.51	0.29
P26583	High mobility group protein B2	0.57	0.05	< 0.01	1.08	0.12	< 0.01	0.79	0.09	< 0.01
P29317	Ephrin type-A receptor 2	0.69	0.14	< 0.01	0.77	0.26	< 0.01	0.88	0.49	0.99
P29558	RNA-binding motif, single-stranded-interacting protein 1	0.54	0.22	0.05	0.62	0.25	0.05	1.53	1.62	0.15
P35080	Profilin-2	0.97	0.21	0.85	0.86	0.27	0.13	0.50	0.26	< 0.01
P35268	60S ribosomal protein L22	0.83	0.08	< 0.01	0.81	0.13	< 0.01	0.65	0.14	< 0.01
P35606	Coatomer subunit beta_	0.50	0.09	< 0.01	0.73	0.23	< 0.01	1.66	2.18	0.34
P35908	Keratin, type II cytoskeletal 2 epidermal	0.62	0.11	< 0.01	1.08	0.23	0.32	0.86	0.21	< 0.01
P38159	Heterogeneous nuclear ribonucleoprotein G	1.41	0.08	< 0.01	1.24	0.12	< 0.01	1.24	0.16	< 0.01
P39748	Flap endonuclease 1	0.92	0.11	< 0.01	0.91	0.16	< 0.01	0.68	0.19	< 0.01
P41567	Eukaryotic translation initiation factor 1	0.54	0.14	< 0.01	0.94	0.33	1.00	0.75	0.53	1.00
P43487	Ran-specific GTPase-activating protein	0.70	0.09	< 0.01	0.93	0.24	0.77	0.87	0.20	< 0.01
P46087	Putative RNA methyltransferase NOL1	0.85	0.05	0.14	0.80	0.12	< 0.01	0.59	0.13	< 0.01
P46779	60S ribosomal protein L28	1.42	0.32	< 0.01	1.27	0.38	0.15	1.05	0.42	< 0.01
P46940	Ras GTPase-activating-like protein IQGAP1	0.92	0.16	0.27	0.93	0.25	0.10	0.71	0.23	0.05
P48634	Large proline-rich protein BAT2	1.48	0.31	0.02	1.37	0.32	0.02	1.15	0.23	< 0.01

P51114	Fragile X mental retardation syndrome-related protein 1	1.48	0.21	< 0.01	1.21	0.33	0.56	1.16	0.32	< 0.01
P52292	Importin subunit alpha-2	0.89	0.02	< 0.01	0.62	0.03	< 0.01	0.80	0.07	< 0.01
P52701	DNA mismatch repair protein Msh6	1.49	0.55	0.02	1.31	0.76	0.47	1.18	0.76	0.03
P52888	Thimet oligopeptidase	0.62	0.16	0.02	0.53	0.13	< 0.01	0.80	0.42	0.99
P57088	Transmembrane protein 33	0.60	0.15	< 0.01	0.97	0.35	0.93	0.62	0.28	< 0.01
P58546	Myotrophin	0.76	0.08	< 0.01	0.66	0.13	< 0.01	0.77	0.33	0.95
P60174	Triosephosphate isomerase	1.20	0.13	0.04	1.44	0.18	< 0.01	1.11	0.17	< 0.01
P60981	Destrin	1.30	0.48	0.50	1.49	0.91	0.26	1.78	1.34	< 0.01
P61513	60S ribosomal protein L37a	0.78	0.10	< 0.01	0.67	0.15	< 0.01	0.68	0.17	< 0.01
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	0.65	0.21	< 0.01	0.52	0.21	< 0.01	0.77	0.35	< 0.01
P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	0.74	0.12	< 0.01	0.70	0.14	< 0.01	0.75	0.23	< 0.01
P62273	40S ribosomal protein S29	0.83	0.08	0.05	0.66	0.12	< 0.01	0.90	0.20	0.12
P62306	Small nuclear ribonucleoprotein F	1.45	0.21	0.03	1.06	0.34	0.91	1.30	0.46	0.03
P62314	Small nuclear ribonucleoprotein Sm D1	1.27	0.19	0.14	1.16	0.20	0.97	1.49	0.69	< 0.01
P62979	40S ribosomal protein S27a	0.57	0.08	< 0.01	0.64	0.22	< 0.01	0.74	0.29	0.34
P62988	Ubiquitin	1.17	0.14	< 0.01	1.22	0.21	0.02	1.56	0.68	< 0.01
P62993	Growth factor receptor-bound protein 2	0.91	0.18	0.03	0.87	0.23	< 0.01	0.71	0.21	< 0.01
P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	0.72	0.09	< 0.01	0.66	0.22	< 0.01	0.84	0.33	0.97
P67809	Nuclease-sensitive element-binding protein 1	0.70	0.03	< 0.01	0.71	0.05	< 0.01	0.78	0.08	< 0.01
P67870	Casein kinase II subunit beta	1.79	0.66	< 0.01	1.34	0.54	0.02	1.23	0.68	< 0.01
P68366	Tubulin alpha-4A chain	0.69	0.03	< 0.01	0.78	0.05	< 0.01	0.85	0.08	< 0.01
P78347	General transcription factor II-I	0.86	0.10	< 0.01	0.81	0.08	< 0.01	0.71	0.13	< 0.01
Q02878	60S ribosomal protein L6	0.83	0.01	< 0.01	1.02	0.09	0.27	0.65	0.08	< 0.01
Q04695	Keratin, type I cytoskeletal 17	0.88	0.06	< 0.01	1.42	0.33	< 0.01	0.78	0.12	< 0.01
Q04837	Single-stranded DNA-binding protein, mitochondrial	0.99	0.23	0.94	0.72	0.20	0.06	0.69	0.38	< 0.01
Q06210	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	1.56	0.31	< 0.01	1.18	0.35	0.30	0.99	0.26	0.21
Q12797	Aspartyl/asparaginyl beta-hydroxylase	1.57	0.58	< 0.01	1.49	0.80	0.07	1.25	0.40	< 0.01
Q12904	Multisynthetase complex auxiliary component p43	1.44	0.37	0.01	1.17	0.25	0.94	1.16	0.48	< 0.01
Q13085	Acetyl-CoA carboxylase 1	1.41	0.62	0.21	0.89	0.52	0.40	1.44	1.10	0.03
Q13151	Heterogeneous nuclear ribonucleoprotein A0	1.42	0.13	< 0.01	1.07	0.17	0.02	1.10	0.28	< 0.01
Q13242	Splicing factor, arginine-serine-rich 9	0.71	0.04	0.01	0.77	0.13	< 0.01	0.68	0.14	0.01
Q13509	Tubulin beta-3 chain	0.74	0.04	< 0.01	0.82	0.06	< 0.01	0.69	0.11	< 0.01
Q13813	Spectrin alpha chain, brain	1.02	0.04	< 0.01	1.01	0.07	< 0.01	0.53	0.07	< 0.01
Q13885	Tubulin beta-2A chain	0.71	0.03	< 0.01	0.79	0.05	< 0.01	0.65	0.09	< 0.01

Q14019	Coactosin-like protein	0.98	0.18	< 0.01	0.69	0.22	< 0.01	1.03	0.30	< 0.01
Q14157	Ubiquitin-associated protein 2-like	0.72	0.04	< 0.01	0.68	0.08	< 0.01	0.88	0.15	0.57
Q14165	Uncharacterized protein KIAA0152	0.46	0.08	< 0.01	0.94	0.24	0.62	0.76	0.35	0.46
Q15185	Prostaglandin E synthase 3	1.23	0.33	0.93	1.01	0.47	1.00	1.41	0.50	< 0.01
Q15631	Translin	1.51	0.48	0.02	1.19	0.46	0.60	1.36	0.90	0.03
Q15637	Splicing factor 1	1.40	0.14	< 0.01	1.28	0.19	< 0.01	1.07	0.27	< 0.01
Q15942	Zyxin	0.63	0.03	< 0.01	0.73	0.04	< 0.01	0.83	0.07	< 0.01
Q16698	2,4-dienoyl-CoA reductase, mitochondrial	0.65	0.52	0.33	0.60	0.47	0.02	1.12	1.41	0.66
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	1.47	0.30	< 0.01	1.19	0.36	0.84	1.21	0.48	< 0.01
Q3MHD2	Protein LSM12 homolog	0.73	0.17	0.07	0.68	0.25	< 0.01	0.72	0.29	0.50
Q53GQ0	Estradiol 17-beta-dehydrogenase 12	1.44	0.21	0.02	1.39	0.25	0.01	1.33	0.43	0.01
Q56VL3	OCIA domain-containing protein 2	1.79	0.68	< 0.01	1.23	0.54	0.70	1.19	1.18	0.40
Q6UY14	ADAMTS-like protein 4	0.83	0.14	0.03	0.70	0.21	< 0.01	0.73	0.28	0.22
Q71DI3	Histone H3.2	0.70	0.07	< 0.01	0.95	0.13	< 0.01	0.85	0.14	< 0.01
Q86YP4	Transcriptional repressor p66-alpha	1.47	0.28	< 0.01	1.15	0.29	0.89	1.06	0.41	< 0.01
Q8IWS0	PHD finger protein 6	1.15	0.21	0.03	0.86	0.26	0.19	0.16	0.12	< 0.01
Q8IY67	Ribonucleoprotein PTB-binding 1	0.66	0.12	< 0.01	0.73	0.21	< 0.01	0.70	0.40	0.53
Q8IY81	Putative rRNA methyltransferase 3	0.57	0.04	< 0.01	0.59	0.06	< 0.01	0.75	0.11	< 0.01
Q8N1F7	Nuclear pore complex protein Nup93	0.98	0.28	1.00	0.82	0.37	0.13	0.47	0.28	0.05
Q8N335	Glycerol-3-phosphate dehydrogenase 1-like protein	1.78	0.40	< 0.01	1.34	0.34	0.13	1.21	0.31	< 0.01
Q8NBS9	Thioredoxin domain-containing protein 5	1.46	0.10	< 0.01	1.15	0.11	0.15	1.01	0.19	0.01
Q92769	Histone deacetylase 2	1.41	0.21	0.01	1.18	0.27	0.86	1.14	0.24	< 0.01
Q96FJ2	Dynein light chain 2, cytoplasmic	1.65	0.28	< 0.01	1.39	0.42	0.05	1.31	0.56	< 0.01
Q96HS1	Phosphoglycerate mutase family member 5	1.45	0.29	< 0.01	1.15	0.27	0.90	1.21	0.31	< 0.01
Q99436	Proteasome subunit beta type-7	1.95	1.21	< 0.01	1.35	0.68	0.09	1.21	0.74	< 0.01
Q9BRA2	Thioredoxin domain-containing protein 17	0.70	0.08	< 0.01	0.80	0.17	< 0.01	0.92	0.33	< 0.01
Q9BRJ6	Uncharacterized protein C7orf50	0.70	0.06	< 0.01	0.75	0.10	< 0.01	0.79	0.14	0.36
Q9BS26	Thioredoxin domain-containing protein 4	0.61	0.21	0.01	0.72	0.24	< 0.01	0.58	0.24	< 0.01
Q9BX5P	Arsenite-resistance protein 2	1.59	0.25	< 0.01	1.20	0.34	0.36	1.09	0.26	< 0.01
Q9BY44	Eukaryotic translation initiation factor 2A	1.29	0.14	0.01	1.20	0.20	0.59	0.64	0.29	< 0.01
Q9C010	cAMP-dependent protein kinase inhibitor beta	1.19	0.27	0.23	1.18	0.44	0.93	1.44	0.82	< 0.01
Q9GZR7	ATP-dependent RNA helicase DDX24	0.65	0.12	< 0.01	0.59	0.29	< 0.01	0.77	0.26	0.43
Q9H0A0	N-acetyltransferase 10	0.69	0.11	< 0.01	0.68	0.13	< 0.01	0.93	0.33	0.76
Q9H444	Charged multivesicular body protein 4b	1.01	0.26	0.99	0.65	0.29	0.07	0.31	0.23	< 0.01
Q9H8Y8	Golgi reassembly-stacking protein 2	0.44	0.12	< 0.01	0.70	0.29	0.02	0.79	0.41	0.63
Q9H910	Hematological and neurological expressed 1-like protein	0.69	0.05	< 0.01	0.75	0.10	< 0.01	0.96	0.13	< 0.01

Q9NS69	Mitochondrial import receptor subunit TOM22 homolog	1.46	0.32	< 0.01	1.06	0.28	1.00	1.07	0.26	< 0.01
Q9NW13	RNA-binding protein 28	0.74	0.12	< 0.01	0.70	0.17	< 0.01	0.85	0.32	0.98
Q9NXH9	N(2),N(2)-dimethylguanosine tRNA methyltransferase	1.63	0.36	< 0.01	1.39	0.39	0.09	1.09	0.37	0.08
Q9UBM7	7-dehydrocholesterol reductase	1.51	0.25	< 0.01	1.22	0.29	0.17	1.12	0.34	0.06
Q9UBT2	SUMO-activating enzyme subunit 2	1.10	0.17	0.98	0.78	0.21	0.30	0.09	0.07	< 0.01
Q9ULV4	Coronin-1C	1.09	0.26	< 0.01	0.92	0.26	0.24	0.65	0.23	< 0.01
Q9Y3D9	28S ribosomal protein S23, mitochondrial	0.69	0.19	0.03	0.94	0.18	0.14	0.81	0.34	0.06
Q9Y5J7	Mitochondrial import inner membrane translocase subunit Tim9	1.54	0.23	< 0.01	1.34	0.29	0.06	1.28	0.35	< 0.01
Q9Y5J9	Mitochondrial import inner membrane translocase subunit Tim8 B	1.39	0.97	0.39	0.62	0.37	0.05	0.82	0.92	0.99
Q9Y6A5	Transforming acidic coiled-coil-containing protein 3	1.77	0.09	< 0.01	1.39	0.29	< 0.01	1.11	0.36	0.07